

REMARKS

Claims 1-12 are pending in the present application.

The rejection of Claims 1-2 under 35 U.S.C. §102(b) over Sloma et al is obviated in part by amendment and traversed in part.

In the outstanding Office Action the Examiner continues to reject the claims over Sloma et al. With respect to Claim 1, the Examiner alleges that the open-ended language of “having” coupled with “one or more” residues to be mutated does not limit the claim to the recited mutations. Applicants continued to disagree with the Examiner’s interpretation, but nonetheless, have replaced the term “having” with “consisting of”. The Examiner’s interpretation and basis for rejecting Claim 1 is thus obviated. Accordingly, the sequence of Sloma et al does not meet the limitations of Claim 1, which requires that the sequence be SEQ ID NO: 1, with the possible specifically recited mutations. As such, Claim 1 cannot be anticipated since all the elements of the claim are not disclosed by Sloma et al.

The Examiner also continues to reject Claim 2 over Sloma et al. In making this rejection, the Examiner alleges that Sloma et al disclose a sequence with 95% homology to SEQ ID NO: 1. Interestingly, recognizing the deficiency in the previous sequence alignment with SEQ ID NO: 42 of Sloma et al (see Office Action mailed April 19, 2006), the Examiner has provided a new sequence alignment of SEQ ID NO: 1 with SEQ ID NO: 42 of Sloma et al in which the alignment parameters have been altered slightly to reveal a “query match” (treated as homology) of 95.0%, rather than the previously reported 94.6%. Be that as it may, this sequence disclosed by Sloma et al still does not anticipate the claimed invention as SEQ ID NO: 42 of Sloma et al is 641 amino acids, while SEQ ID NO: 1 of the present invention is only 434 amino acids. As such, even if SEQ ID NO: 42 of Sloma et al is 95.0% homologous

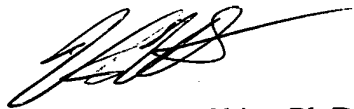
over a 434 amino acid internal fragment, the actual homology between this sequence and SEQ ID NO: 1 would be based on the full-length protein. As such, the proper degree of homology between SEQ ID NO: 42 of Sloma et al and SEQ ID NO: 1 of the present invention is calculated as:  $(407/641) * 100 = 63.5\%$ . Therefore, Sloma et al clearly does not anticipate Claim 2.

In view of the foregoing, Applicants request withdrawal of this ground of rejection.

Accordingly, Applicants submit that the present application is now in condition for allowance. Early notification of such action is earnestly solicited.

Respectfully submitted,

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